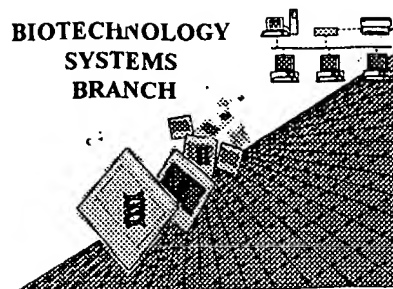# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/671,687_

Source: _BATCH - RUSH_

Date Processed by STIC: _3/29/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable Form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/671,687_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                This may occur if your file was retrieved in a word processor after creating it.
                                Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                                This may occur if your file was retrieved in a word processor after creating it.
                                Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
        Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                               Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                               As per the rules, each n or Xaa can only represent a single residue.
                               Please present the maximum number of each residue having variable length and
                               indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                               sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                               to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
                               sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
        (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                               (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                               This sequence is intentionally skipped

                               Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                               <400> sequence id number
                               000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
        (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
        (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                               Please explain source of genetic material in <220> to <223> section.
                               (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
                               file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                               Instead, please use "File Manager" or any other means to copy file to floppy disk.

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        RAW SEQUENCE LISTING                DATE: 03/29/2001
        PATENT APPLICATION:  US/09/671,687  TIME: 09:34:53

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            Output Set: N:\CRF3\03292001\I671687.raw
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Does Not Comply
Corrected Diskette Needed

pp 1-2

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     3 <110> APPLICANT: WALLACH, David
     4        KOVALENKO, Andrei
     5        CANTARELLA, Giuseppina
     7 <120> TITLE OF INVENTION: Inhibitor of NF-kB Activator
     9 <130> FILE REFERENCE: WALLACH=25
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    12 <141> CURRENT FILING DATE: 2000-09-28
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    15 <151> PRIOR FILING DATE: 1999-03-18
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    23 <150> PRIOR APPLICATION NUMBER: IL 134604
    24 <151> PRIOR FILING DATE: 2000-02-17
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W--> 45 (handwritten circles on sequence)
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see item 10 on Error Summary Sheet

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Output Set: N:\CRF3\03292001\I671687.raw

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001
TIME: 09:34:54

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Output Set: **N:\CRF3\03292001\I671687.raw**

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L:45  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:45  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:46  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:46  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:46  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:46  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:47  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:47  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:47  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:47  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:79  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:79  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:79  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:79  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:79  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:91  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:91  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:91  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:91  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:101 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
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